

C	anti-CD3	anti-CD16	anti-CD158 (p50.1, EB6)	anti-CD158 (p50.2, C1.18.3)	anti-CD158 (p50.3, PAX250)

Relative number of cells

三

126

三

171

Intensity of fluorescence

Vijanti

Figure 1B

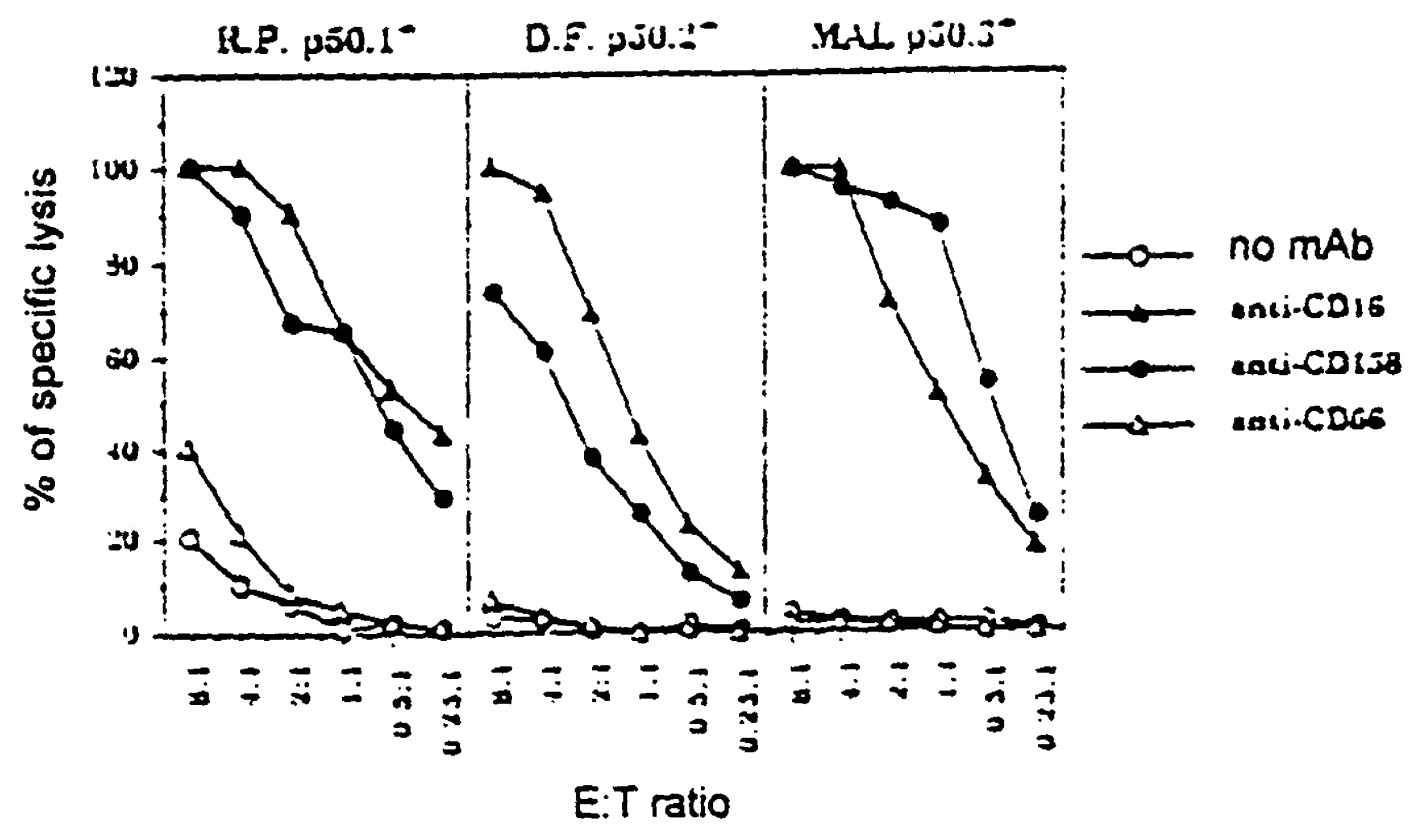


Figure 2A

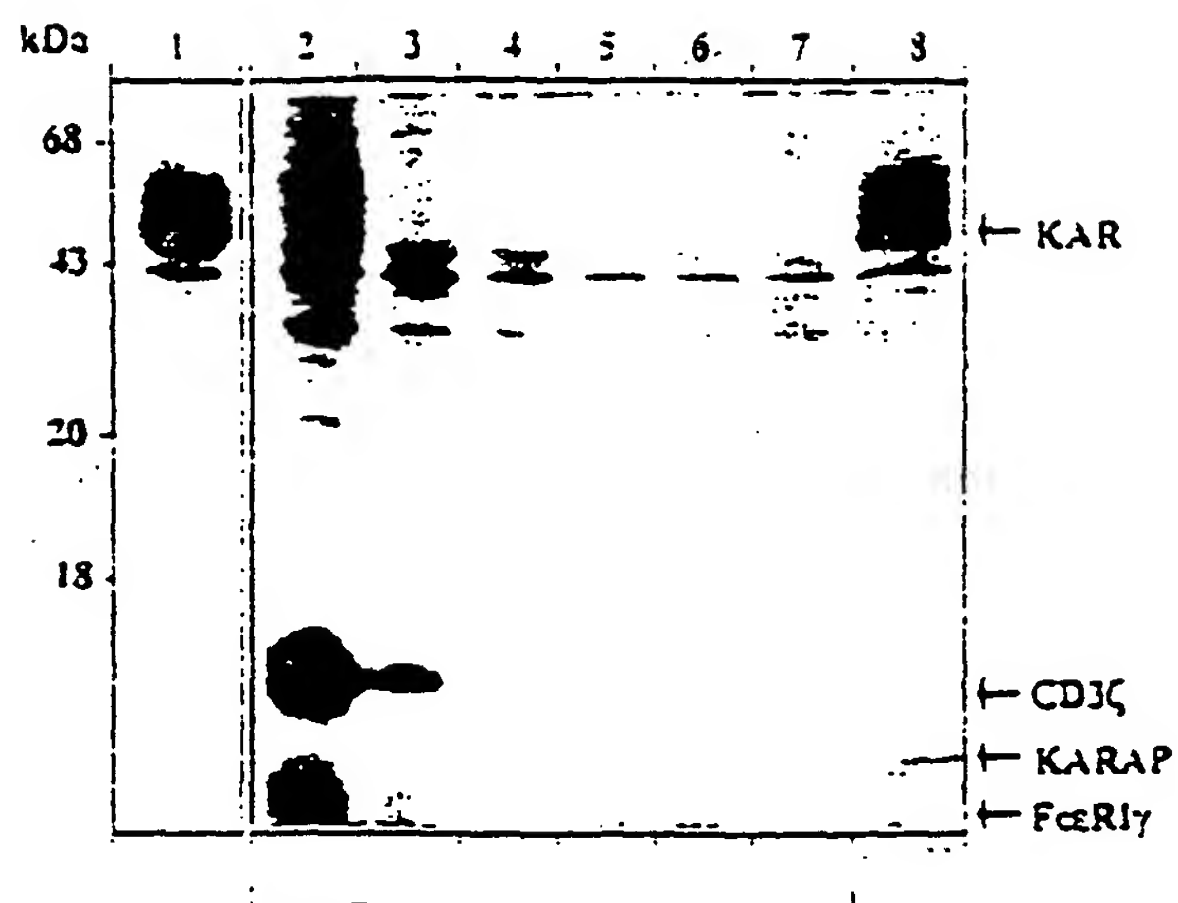


Figure 2B



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Figure 3A

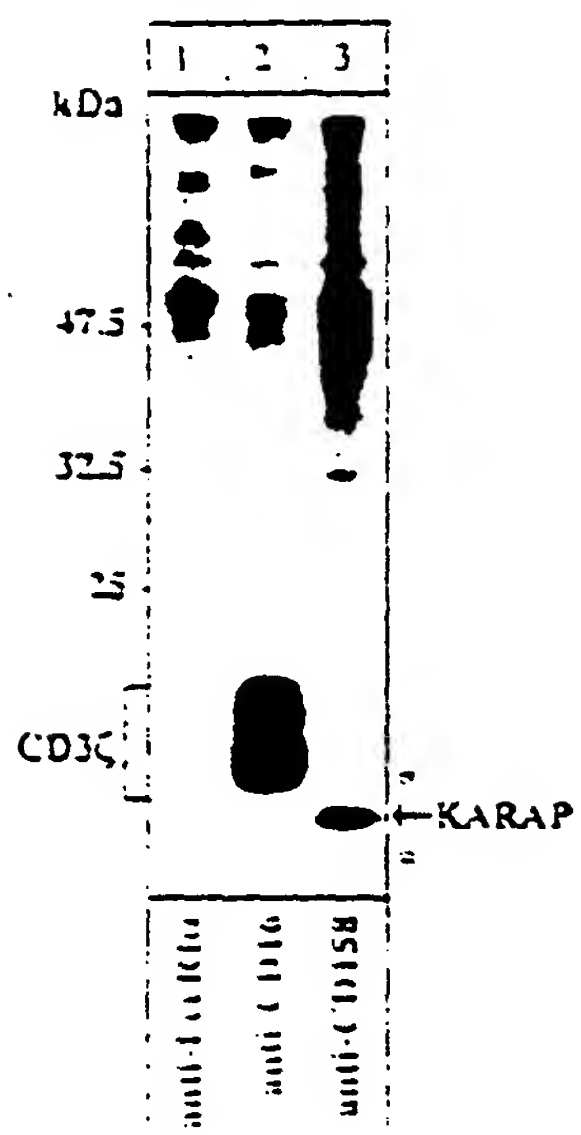


Figure 3B

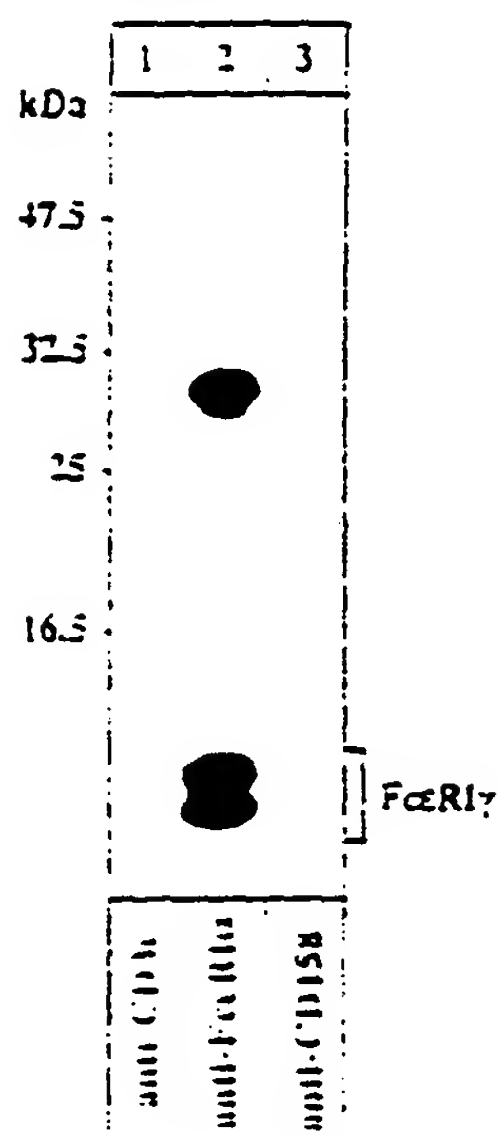
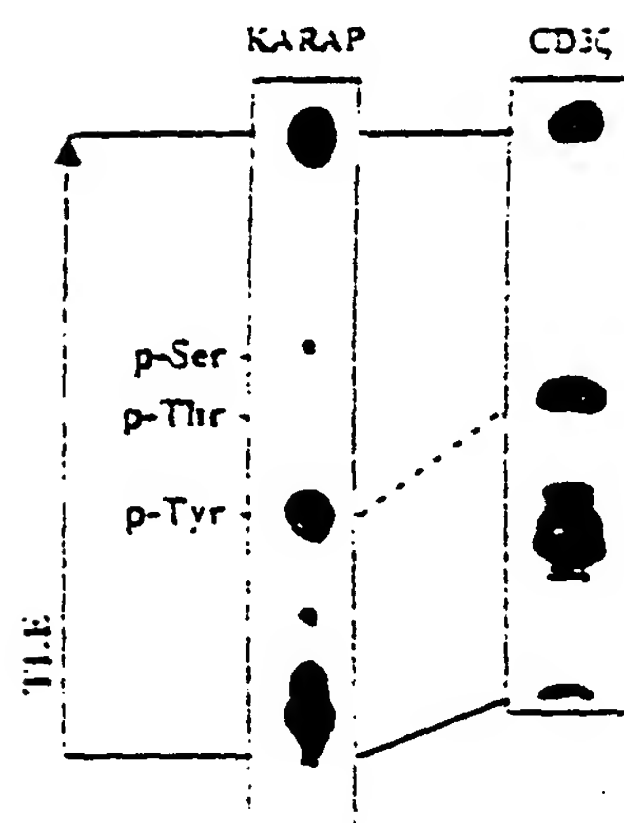
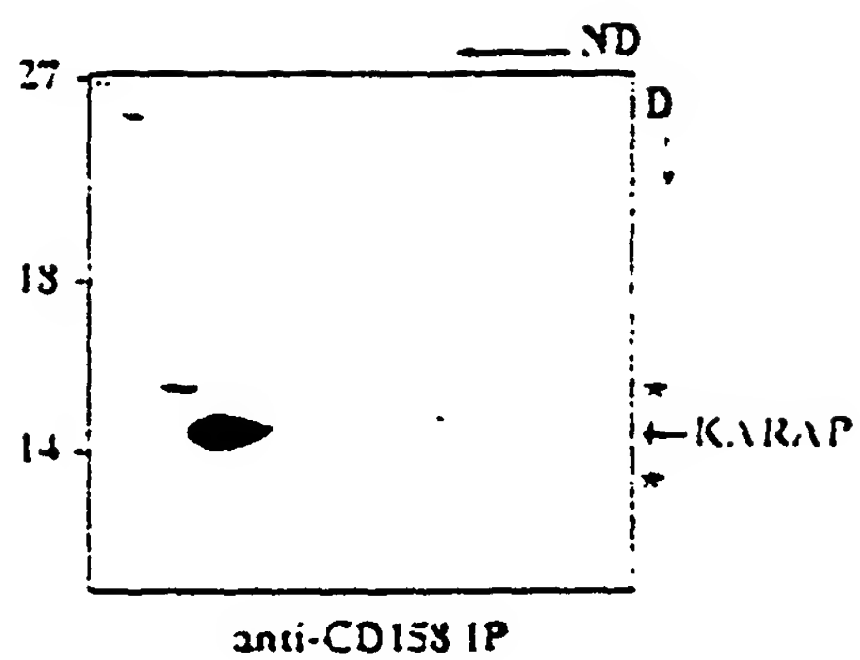


Figure 3C



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Figure 4

NK p58/50 cell receptors for class I MHC molecules

Figure 6

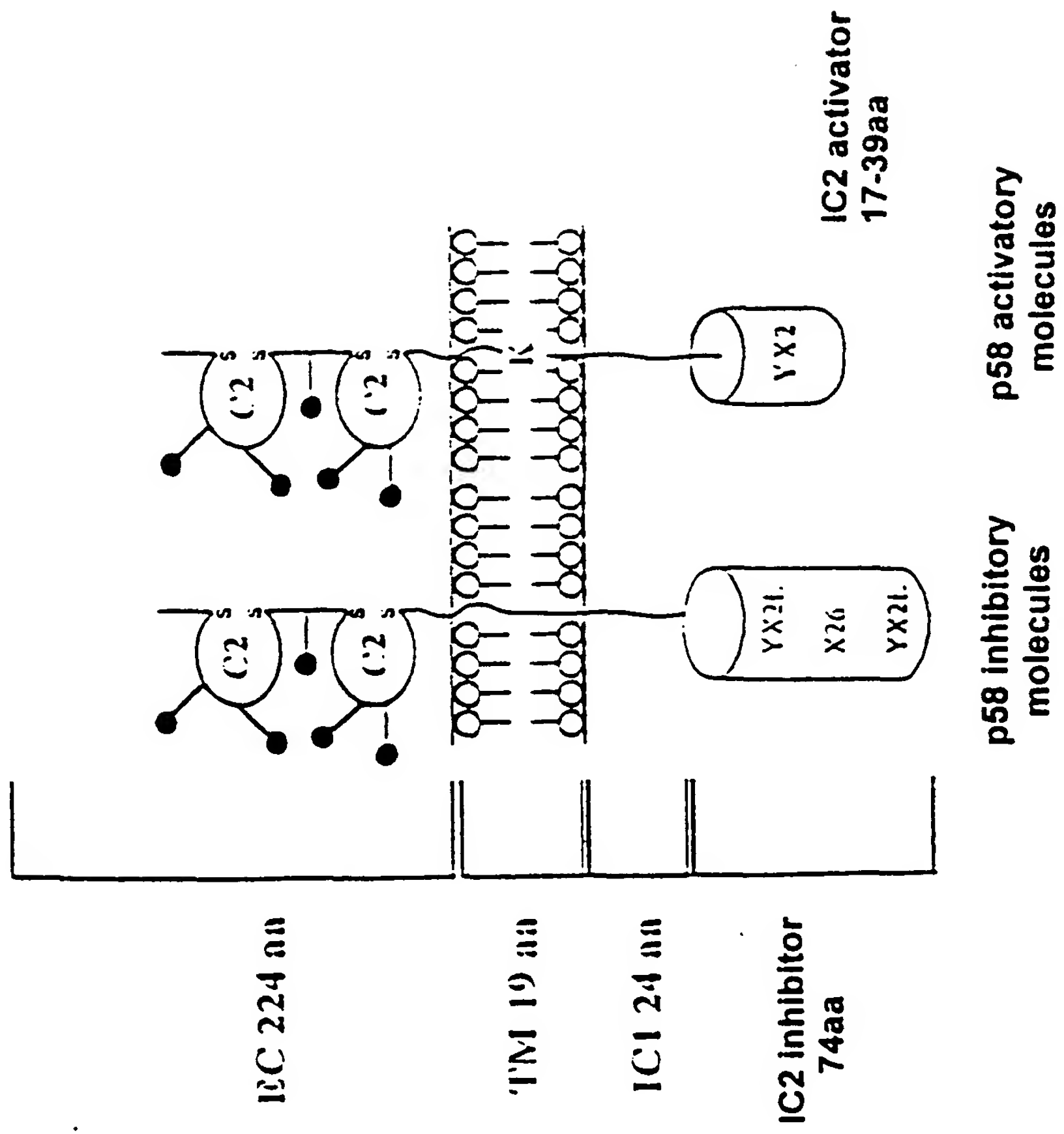


Figure 7

1 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 61 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 121 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 181 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 241 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 301 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 361 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 421 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA
 481 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA 5'GTCACACCA 3'GTCACACCA

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9/26

Plumbea

1/1

31/11

020 200 020 200 000 000 200 200 020 020 000 000 020 200 000 020 020 000 020 020
Q S D T F P R C D C S S V S P G V L S G

61/21

91/31

200 020 020 020 020 020 020 020 200 020 020 200 000 020 020 020 020 020 020 020
I V L G D L V L T L L I A L A V Y S L G

121/41

151/51

020 020 020 000 020 020 020 020 200 020 020 020 020 200 020 020 020 020 020 020
R L V S R G L G T A E G T R X Q E I A E

181/61

211/71

200 020 020 000 020 020 020 020 020 020 020 200 020 020 020 020 020 020 020
T E S P Y Q E L L G C R E E V Y S D L N

241/81

200 020 200 020 020 020 200

T Q R Q Y Y R

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Figure 3

ITAM polypeptides	
$\alpha 3\zeta_1$	YneInlgrrae-YdrL
$\alpha 3\zeta_2$	YneLqkckmaaaYseL
$\alpha 3\zeta_3$	YggLstarkot-YdaL
$\alpha 3\gamma$	YqyLkcreddq-YshL
$\alpha 3\delta$	YqyLrrrdcaq-YshL
$\alpha 3\epsilon$	YqyLrkqqrnl-YsgL
IgG ($\alpha 7Sa$)	YedLsnglqqr-YqdY
IgG ($\alpha 7Sb$)	YqyLdlcqtat-YedL
$\alpha 2\gamma$	YqyLdringat-YatL
$\alpha 2\zeta$	YeeLnlyeat--YseL
$\alpha 3\zeta$	YqyLqgqrnar-YsdL
Consensus	Y--L-----Y--L

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Figure 10A

SEQ ID n°6

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TCACCTCTGG	TTCGACAGT	CGTCGCTG	TGCTCTCTG	TGCTCTCTG	50
GGCAGCTGG	GGCTCTGG	CGCTCTGG	CGCTCTGG	CGCTCTGG	100
TCTCTCTCT	GGCAGCTG	ATCTCTCT	AGCTCTCT	TGCTCTCT	150
CGCTCTCT	ATCTCTCT	CGCTCTCT	CGCTCTCT	CGCTCTCT	200
TGCTCTCT	TGCTCTCT	CGCTCTCT	TGCTCTCT	CGCTCTCT	250
TGCTCTCT	CGCTCTCT	CGCTCTCT	CGCTCTCT	CGCTCTCT	300
CGCTCTCT	CGCTCTCT	CGCTCTCT	CGCTCTCT	CGCTCTCT	350
ATCTCTCT	TGCTCTCT	TGCTCTCT	CGCTCTCT	TGCTCTCT	400
CGCTCTCT	CGCTCTCT	CGCTCTCT	CGCTCTCT	TGCTCTCT	450
TGCTCTCT	ATCTCTCT	TGCTCTCT	CGCTCTCT	TGCTCTCT	500
ATCTCTCT	TGCTCTCT				550

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
SHYVFPPE	NPVFPPEP	GGGSCVLE	LPVFPPEP	SPVFPPEP	50
FPVFPPEP	GVLSGVLE	LVFPPEP	VFPPEP	GVFPPEP	100
GVFPPEP	GVFPPEP	VFPPEP	VFPPEP	GVFPPEP	150
GVFPPEP	GVFPPEP				171

Figure 10B

SEQ ID n°11

Figure 11A

SEQ ID n°7

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GTGGCTCTT	GGGACCGAG	GGGGCTGAG	AGGCTGCTG	GTGGCTCTG	50
TTCCTTCCTG	TCTCTCTGAC	TGTTGGTGG	TTCAGTCTCG	TACGCTCCCA	100
GTGCTCTCT	TTCCTCTGAG	GGGCTCTCT	TTCCTCTCTG	CTGCTCTCTG	150
TCTCTCTCT	TCTCTCTCT	GCTCTCTCT	TCTCTCTCT	GCTCTCTCT	200
CTGCTCTCT	CTGCTCTCT	CTGCTCTCT	CTGCTCTCT	GGCTCTCTG	250
AGGCTCTCT	AGGCTCTCT	TCTCTCTCT	TCTCTCTCT	TCTCTCTCT	300
TCTCTCTCT	GCTCTCTCT	GCTCTCTCT	AGGCTCTCT	AGGCTCTCT	350
TCTCTCTCT	GCTCTCTCT	T			371

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
ATATATGCT	TTATATATAT	TTATATATAT	CAATATATAT	CAATATATAT	50
ATATATATAT	TTATATATAT	ATATATATAT	ATATATATAT	ATATATATAT	100
CAATATATAT	ATATATATAT	ATATATATAT			123

Figure 11B

SEQ ID n°12

Figure 12A

SEQ ID n°8

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GCTTTTGGT	CTTTCCTGTC	CTTTCGACTG	TGGGAGATT	AAGTCCCGTA	50
CTGCGCTGCA	GAGAGATT	CCCAAGATG	CGCTGATTT	CGCTGAGCCC	100
TGTTTACTG	GCTGGGATG	TTTGGGATG	CTTGGGATG	AATGCTGCTA	150
TTGCTTGGT	TGCTGATTT	CTGCGCGCC	TGCTTCCCG	AAGTCTAGCG	200
AAGCGGTA	CGCGCGTA	AATAGCTT	GCTGAGCTG	AATGCGCTA	250
TGCTGATTT	CGCGCTGCA	GCTGAGAT	AATAGCTA	CTCAAGCTC	300
AATGCTA	TTCTGCTA	GCTGATTT	TGCTGCTA	CGCGCTGCTG	350
CGCGCTGCTG	GCTGCTGCTG	AATCT			375

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTTCTTCTT	CGCTGCTGCA	CTTCTGCTG	CTTCTGCTG	CTTCTGCTG	50
CTTCTGCTG	CTTCTGCTG	CTTCTGCTG	CTTCTGCTG	CTTCTGCTG	100
CTTCTGCTG	CTTCTGCTG	CTTCTGCTG	CTTCTGCTG	CTTCTGCTG	124

Figure 12B

SEQ ID n°13

SEQ ID n°9

Figure 13A

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CGAGGCGGCG	GAATGGGGG	TGCAATGCG	ATGAGGCGCG	CGTGGGGCG	5
CTGGAGCGCG	CTGGAGCGCG	CTGGAGCGCG	CTGGAGCGCG	GAATGGGGG	100
CGATGAGCG	CGATGAGCG	CGATGAGCG	ATGAGGCGCG	GAATGGGGG	150
TGATGCGCG	AGGCGGGCG	TGATGCGCG	GAATGGGGG	CGTGGGGCG	200
TGATGCGCG	CGTGGGGCG	CGTGGGGCG	ATGAGGCGCG	CGGCGGGCG	250
TGATGCGCG	AGGCGGGCG	CGATGAGCG	CGATGAGCG	AGTGGGGCG	300
GAATGGGGG	CGATGAGCG	AGTGGGGCG	TGATGAGCG	GAATGGGGG	350
GTGAGGCGCG	CGATGAGCG	CGATGAGCG	GAATGGGGG	TGATGAGCG	400
CGATGAGCG	CGATGAGCG	CGATGAGCG	GAATGGGGG	TGATGAGCG	450

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
QFLDGGVQCI	SGHGGGGAS	AGLFLVAV	TGELSPVQA	QSDTFFFGCC	5
SS/SEGVLAG	WAGLVAV	AGLFLVAV	FLVFGQQA	SGHGGGGAS	100
TGELSPVQA	QFLDGGVQCI	SGHGGGGAS	AGLFLVAV	QSDTFFFGCC	150

Figure 13B

SEQ ID n°14

Figure 14A

SEQ ID n°10

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GTTCCTTCCT	GTTCCTTCCT	GTTCCTTCCT	GTTCCTTCCT	GTTCCTTCCT	50
ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	100
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	150
GGTCCTTC	GGTCCTTC	GGTCCTTC	GGTCCTTC	GGTCCTTC	200
ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	250
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	300
ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	350
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	400
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	450
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	500

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	50
ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	ATGTCCTTC	100
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	150
CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	CTGTCCTTC	200

Figure 14B

SEQ ID n°15

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Page	Line	Account	Amount	Balance	Debit	Credit
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1	2	10000000	10000000	10000000		
1	3	10000000	10000000	10000000		
1	4	10000000	10000000	10000000		
1	5	10000000	10000000	10000000		
1	6	10000000	10000000	10000000		
1	7	10000000	10000000	10000000		
1	8	10000000	10000000	10000000		
1	9	10000000	10000000	10000000		
1	10	10000000	10000000	10000000		
1	11	10000000	10000000	10000000		
1	12	10000000	10000000	10000000		
1	13	10000000	10000000	10000000		
1	14	10000000	10000000	10000000		
1	15	10000000	10000000	10000000		
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1	18	10000000	10000000	10000000		
1	19	10000000	10000000	10000000		
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1	21	10000000	10000000	10000000		
1	22	10000000	10000000	10000000		
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1	25	10000000	10000000	10000000		
1	26	10000000	10000000	10000000		
1	27	10000000	10000000	10000000		
1	28	10000000	10000000	10000000		
1	29	10000000	10000000	10000000		
1	30	10000000	10000000	10000000		
1	31	10000000	10000000	10000000		
1	32	10000000	10000000	10000000		
1	33	10000000	10000000	10000000		
1	34	10000000	10000000	10000000		
1	35	10000000	10000000	10000000		
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1	38	10000000	10000000	10000000		
1	39	10000000	10000000	10000000		
1	40	10000000	10000000	10000000		
1	41	10000000	10000000	10000000		
1	42	10000000	10000000	10000000		
1	43	10000000	10000000	10000000		
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1	49	10000000	10000000	10000000		
1	50	10000000	10000000	10000000		
1	51	10000000	10000000	10000000		
1	52	10000000	10000000	10000000		
1	53	10000000	10000000	10000000		
1	54	10000000	10000000	10000000		
1	55	10000000	10			






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Figure 15 (contd.)

AA093506	402
AA242313	402
W83159	373
AA734769	371
W41142	402
Consensus	AGCCGCTCT	AGCCGCTCA	GGGCGTGT	GGCGGCTCC	GCTCATTCG	450
AA093506	402
AA242313G..A..	402
W83159	373
AA734769	371
W41142G..G..	402
Consensus	GTGCGTCTCT	GTACAGCCC	TTCTSTGCA	TCGCGCTCC	GCTTCGACA	500
AA093506	402
AA242313	402
W83159	373
AA734769	371
W41142	402
Consensus	CGATTCGCA	GGTACTTCC	CTGAGATTC	TCGATTCGA	CGATTCGCA	550
AA093506	402
AA242313	402
W83159	373
AA734769	371
W41142	402
Consensus	CCCCAATAG	AAGACCGCA	570

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Figure 16

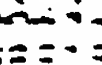
SEQ ID n°11  protein
 SEQ ID n°13  protein
 SEQ ID n°15  protein
 SEQ ID n°14  protein
 SEQ ID n°12  protein

SEQ ID n°17

A21402.13 protein
 A21403.13 protein
 A21404.13 protein
 A21405.13 protein
 A21406.13 protein

Conclusion

Conclusions



செய்துரை:

SECURITY POL	SECURITY POL	SECURITY POL			
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OFFICE OF	SECURITY	SECURITY			
AND	AND	AND			
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[illegible][illegible]

[illegible]

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Figure 17 (contd.)

SEQ ID n° 18 (contd.)

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGGCTGGG	AGGAGCGT	GTGTCGAC	AAAGAGGA	ACGAAAGCA	2100
AAGGAGGA	AAAGAGTT	CAATTCGG	GGCTGAGT	CGAGAGAG	2150
CGGGGCTG	CTATTAGA	GAGCGGGA	ATTTCAGG	AAAGTCAG	2200
CTGTTTTT	GTGCTGGG	TGCTTCGT	GGGCTGAG	TGGTCAGA	2250
CGGCTGCA	ATTGAGAG	CTTATTGA	GGATTGAC	AAAGCGTT	2300
GGGTCAGT	TATAGAGA	TGATATGA	CGATGATG	GGTGGGCG	2350
GAAGGAGT	GAATTCGG	AACTAAGG	ATTGCTAG	CTGAAAGG	2400
GGGCTGTC	AGATTCGG	CGTTGGTG	TGAGGCTG	GGGTCGGG	2450
GGTGCAGT	TAGTCGCT	GGGTCGGT	CTATGTCG	AGGTGAAAG	2500
GGTGGGGA	TGATGCTG	ATTTCATG	ATTTCAGT	TTTTCAGT	2550
TTTTCAGT	AAATGCTG	CGGTCGTT	GAATGCTT	AGTTCGCT	2600
ATTTCAGT	ATTTCGCG	CGGTCGTA	TGATGCTT	TTTTCAGT	2650
TTTTCAGT	TGATGCTG	CGGTCGTA	GGTTCGTT	ATTTCAGT	2700
AGTTCGGA	TATTCAGT	GGGTCGTT	TGATGCTT	AGGTCGCT	2750
TGATGCTT	CGGTCGTT	AGTTCGTA	TGATGCTT	CTTTCAGT	2800
TGATGCTT	CGGTCGTA	CGGTCGTA	CGGTCGTT		2850

Figure 13

3' Intron sequence
(donor site)

Exon sequence

5' Intron sequence
(acceptor site)

MetGly LeuGlu
ATGGGG...-Exon 1-...TCCAGG

GAGGTGA....

....TCCCTAG

IleLeu LeuGlu
GATTAA...-Exon 2-...ACAGTG

GTAAGCC...

....TCCCTAG

LeuLeu LeuGlu
ACACTT...-Exon 3-...AACAGA

GTAAGAA...

....TCCCTAG

LeuLeu TyrGlu
GGACCC...-Exon 4-...TATCAG

GTAAGAA....

....TTCCTAG

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Figure 19

	10	20	30	40	50	
	101456789	101456789	101456789	101456789	101456789	
SEQ ID n°27	ATGGGGGCTC	TGAAGCCCTC	CTGGTGGCTT	CTGTTGCTTC	CTGTCCCTCCT	30
SEQ ID n°28	M G A L E P S W C L L F L P Y L L					
	GACTGTGGAG	GCAATTAAGTC	CCCTAAGCC	CCAGAGTGAC	ACTTTCCCA	100
	T V E G L S P Y Q A L S D T F P E					
	GATGCGACTC	TTCTTCCCTG	AGCCCTGCTG	TACTTGCCTG	GATTCTTCTG	150
	C D C S S V S P G V L A G I V L					
	GCTGACTTGG	TCTTAAGTCT	GCTGATTGCC	CTGGCTGTCT	ACTCTCTGGG	200
	G D L V L T L L T A L A Y Y S L G					
	CCGCTCTGTC	TCCCGAGCTC	ACGAGAGGAC	CCGAAACAA	CACATTGCTG	250
	R L V S R G Q E R T R E Q H I A E					
	AGCTGAGTTC	GCTTATCAG	GAGTTTCAAG	GTGAGAGACA	TGAGTATAC	300
	T E S P Y Q E L Q G Q R H E V Y					
	AGTGAATCTA	ACAGCAGAG	GCAATATTAC	AGTGAATCCC	ACTTATATGC	350
	S D L N T Q R Q Y Y R A H S M P					
	CATCAGCCGC	CTGATGCCCG	GATCCGCTCA	TTCCAGATCC	CTACTCAACA	400
	I S G L H P G S G H S R C L L N K					
	AGCTCTCTCT	GAGATCAGGA	CTCCCTTTGG	AAACAGATTC	CACGGGTAC	450
	P S L R S G L P L E Y R S T G Y					
						452

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Figure 20

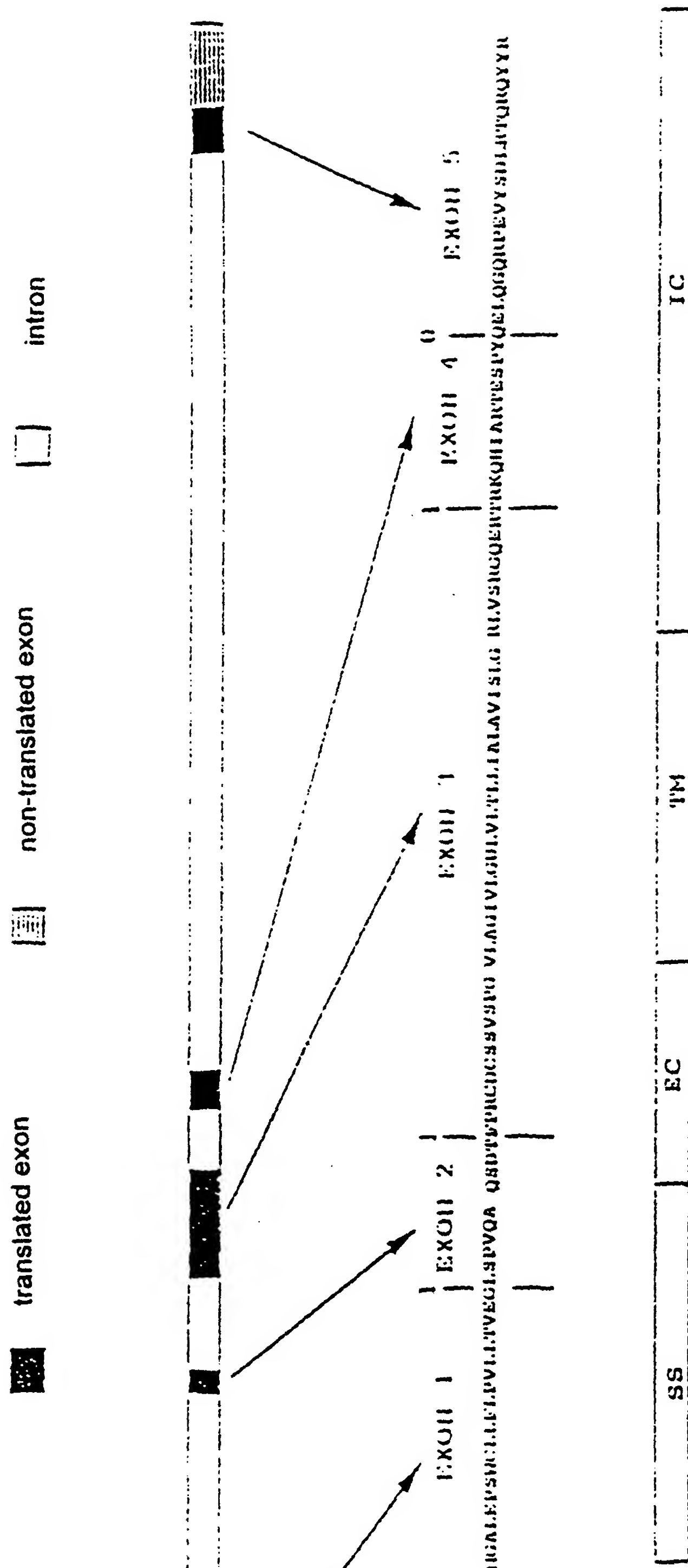


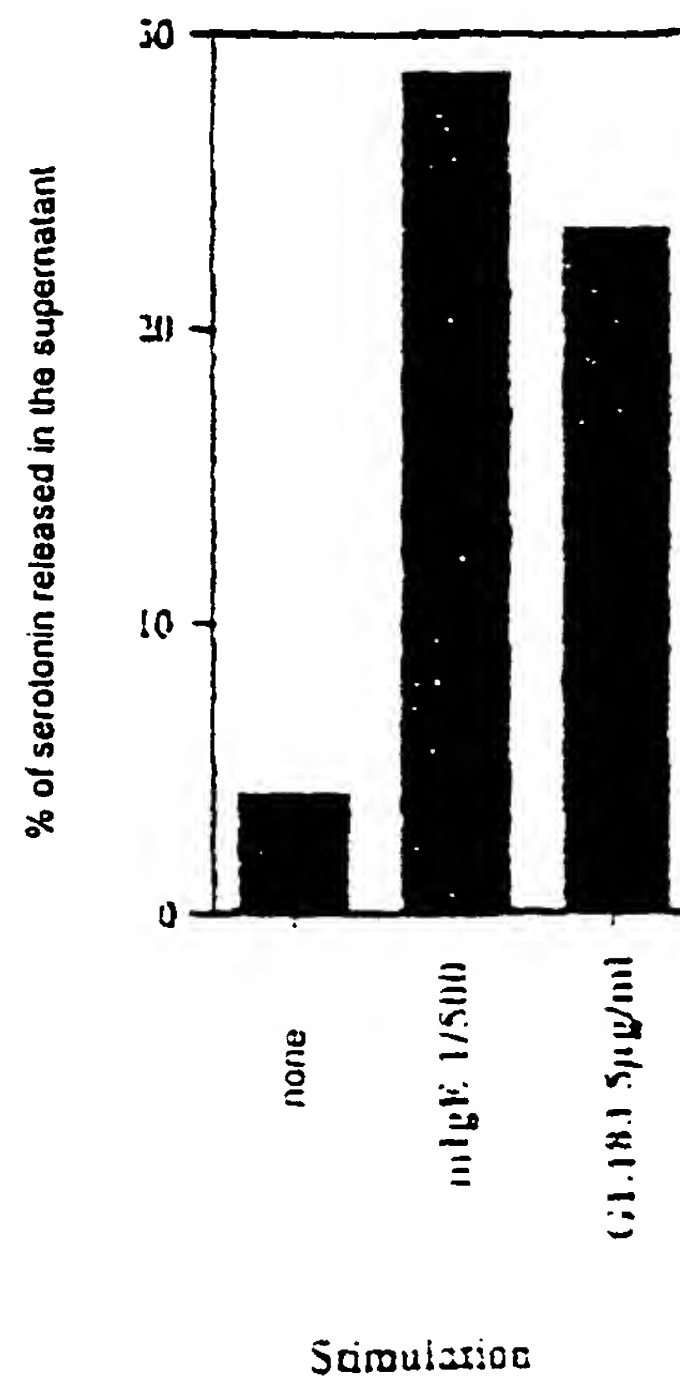
Figure 21

SEQ ID n°31

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGGTCGGT	TGGTTCCT	GGGTCGGT	ATGCAAGTC	CTGGTGGCT	5
TGGTGGGG	ACTTGAAGC	TGGTGGGG	TGGTGGGG	GGTGGGG	100
Low Initiation					
GGGTCGGT	GGGTCGGT	TGGTGGGG	GGGTCGGT	ACTTGAAGC	150
GGTGGGG	ACTTGAAGC	GGGTCGGT	GGGTCGGT	GGTGGGG	200
ACTTGAAGC	GGGTCGGT	ACTTGAAGC	GGGTCGGT	GGGTCGGT	250
GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	300
GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	350
GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	400
Stop					
GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	GGGTCGGT	451

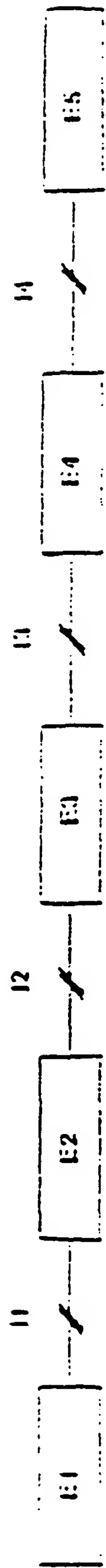
Figure 22

**Release of serotonin induced by the p50/KARAP
complex reconstituted in RBL-2H3 cells**



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Figure 23



26/26

> 65 human KARAP

2302

46

1800

134

140

30

404

62

> 102 murine KARAP

1666

43

91

130

144

31

440

116